

Fig. 1A

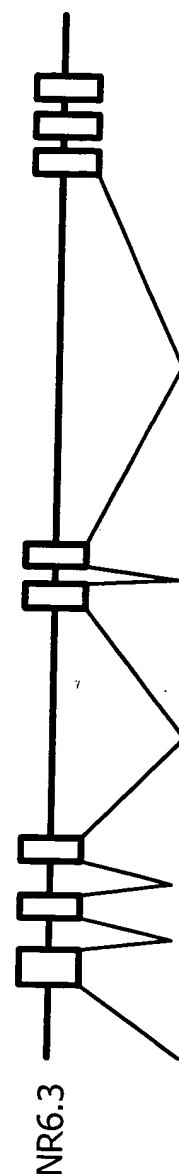
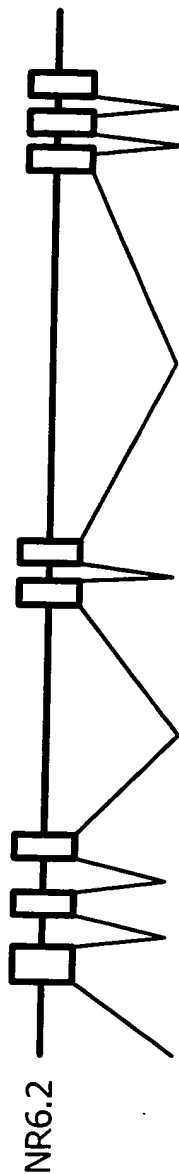
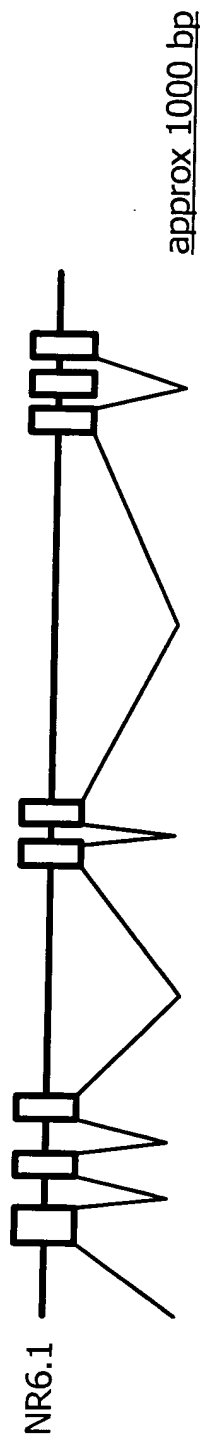


Fig. 1B

NOVEL HAEMOPOLYMERIN RECEPTOR
AND GENETIC SEQUENCES
ENCODING SAME
Douglas J. Hilton, et al.
U.S. Serial No. 09/037,657
REPLACEMENT SHEET

g1	cccagaactcttggacgctgagggcaggaggattccca
g38	agtttcaagacagtgtgtttctaggtaatgagaccctgtcaagaa
g83	aagaaaagaaataaagagacaagaaaatgtttataggctgtgaga
g128	cagcttgggtgggtaaggggcaacttgccccaatcaagatgacctc
g173	agcccccattccctaggaatccatggtagaaggagaaagcaaactcg
g218	cagctgctgacctccatacatgtgctccaatgtgacacacacacag
g263	ggagacataatcaattaataggatgtatttgcttagatttgagta
g308	ggcatttatgactgatgttttaaaatttttatttgattttatgaa
g353	aatataacctgtttgtatttggtttgggtttgagttttgttt
g398	atttgagacagggcttctctgtgtagtcctggctgtccttggaac
g443	tcactctgtagaccaggctggccttgaactcagaaatccgcctgc
g488	ttgtgcttcccaagtgttagattaaagggtgtgcaactgccattca
g533	gcaaaattgcatactttaaccccagtaatttgggaggcagaggcag
g578	actaatgtgtgaattccaggctagccaaggatacagagtgagacc
g623	ctattcttaccctcccccccccaaaacccccaaaatgtattttgtgc
g668	ttgtgtatgtacatgtgtgttgacgacgtaaatgtccaaggaca
g713	acttgtagaagttctctccgttcacagtetaagtccctgaattcaa
g758	actaaggctcctcaggcttagccacagtcttctttatgtactgagc
g803	catttcactggccctggattgactgatgaattaatttttgagata
g848	aggtctcttgtagctctagctaggctcaaactatgaactcccaag
g893	gtcatcttgagctgctggtactcttgcttccacccaagtgggtgg
g938	aatgatactcaggcagcacttctctggggaaggggctggccttgg
g983	ccttgattttgttgacctcagcttcaatgagtgttgggtctcgtt
g1028	gtttcttttctttatctgtgaaatgggtgaacacctgttcaagac
g1073	ttcctgactcttgaaacatccaggcagggtgagggacttgaagtg

A- . - . - . - . - . - . - . - . - A

Fig. 2(1)

A- A

g1118 ggctcatcccatgcctaacaaagtgtcgtcttttgaccccagacac
D P T L L I G S S

g1163 agctgtaatcagccccccagGACCCCACCCTTCTCATCGGCTCCTC

g1208 L Q A T C S I H G D T P G A T
CCTGCAAGCTACCTGCTCTATACATGGAGACACACCTGGGGCCAC

g1253 A E G L Y W T F N G R R L P S
CGCTGAGGGGCTCTACTGGACCTTCAATGGTCGCCGCCTGCCCTC

g1298 E L S R L L N T S T L A L A L
TGAGCTGTCCCGCCTCCTTAACACCTCCACCCTGGCCCTGGCCCT

g1343 A N L N G S R Q Q S G D N L V
GGCTAACCTTAATGGGTCCAGGCAGCAGTCAGGAGACAATCTGGT

g1388 C H A R D G S I L A G S C L Y
GTGTCAGGCCCGAGACGGCAGCATTCTGGCTGGCTCCTGCCTCTA
V G

g1433 TGTGCTgtaagtggggccccagacactcagagatagatggggg

g1478 ttggcaatgacagatttagagcctgggtcttctgtcctggggcag

g1523 agccatgggctctcacttgcattgcaggcatgggtcataccagcac

g1568 aggcattgcaactctagggacagctgtggctgcactgtccctgt

g1613 L
gtacccacagctttagaaaagctgtcatgttttctttagTGC

B- B

Fig. 2(2)

B- . - . - . - . - . - . - . - . B

C- . - . - . - . - . - . - . - . C

Fig. 2(3)

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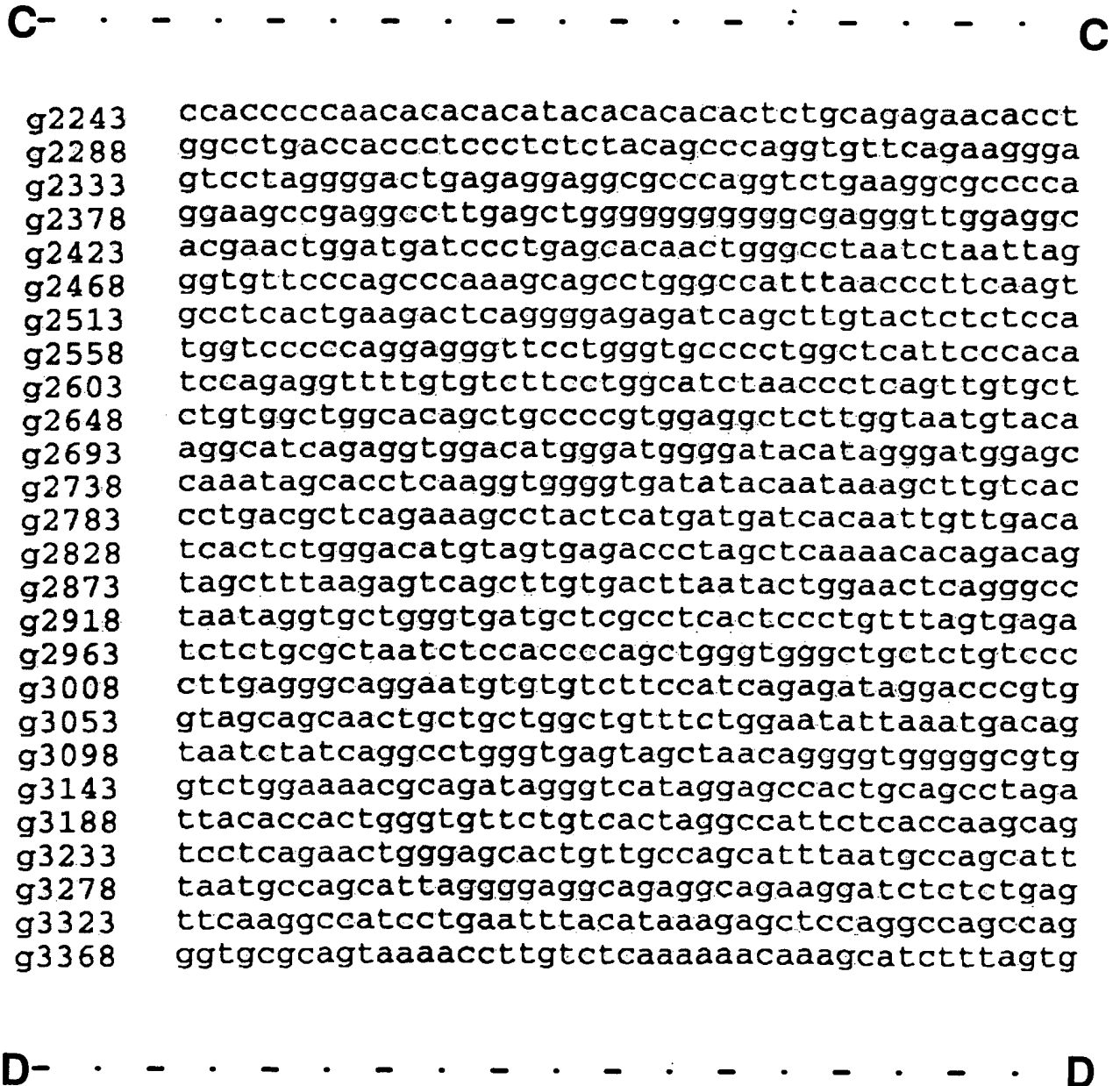


Fig. 2(4)

D- D

g3413 accagggttgctccacccccagTGACCACGGACCCCCACCCGAC

g3458 V H V S R V G G L E D Q L S V
GTGCACGTGAGCCGCGTTGGGGGCCTGGAGGACCAGCTGAGTGTg

g3503 R W V S P P A L K D F L F Q A
CGCTGGGTCTCACCACCAGCTCTCAAGGATTTCTCTTCCAAGCC

g3548 K Y Q I R Y R V E D S V D W K
AAGTACCAGATCCGCTACCGCGTGGAGGACAGCGTGGACTGGAAG

g3593 gtgcccgtcccgcggcccgacccgcccctgaccccgccccccgcat

g3638 V V D D V S N
ctgactcctccctcaccgtgcagGTGGTCGATGACGTCAGCAACC

g3683 Q T S C R L A G L K P G T V Y
AGACCTCCTGCCGTCTCGCGGGCCTGAAGCCCGGCACCGTTTACT

g3728 F V Q V R C N P F G I Y G S K
TCGTCCAAGTGCCTTGTAACCCATTTCGGGATCTATGGGTGCAAAA

g3773 K A G I W S E W S H P T A A S
AGGCGGGAATCTGGAGCGAGTGGAGCCACCCACCGCTGCCTCCA

g3818 T P R S
CCCCTCGAAGTGgtgagcacctctccagggtggtggtggcccatgg

g3863 aatcccgaatccatcctgttccttcccccccaccctttttttgag

E- E

Fig. 2(5)

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E- E

g3908	acagcgtcttcaggtagcgcacatgctggccttaaattcagtatgta
g3953	gtcaaggatgacctcgagctcctggctcttttgtctccacttaga
g3998	gacaatggccagtggccatcaccaccttggggagactagccatgg
g4043	agtctatttagcctgtcatttgggtgacagatggagtacaacagtg
g4088	tgacctcttgtaagagaactgaagacaggctgtttttaaccccaa
g4133	tatcctaggctctctagagggttaactttatataaaaatagagacta
g4178	ttacagccagttatcacatggteccacagaaccttttgtcacaca
g4223	acctatagaccacagtgcctgtgcctaceacataaggggtctctac
g4268	tgctggcccacccctccaaccttaaaaggtaacctaggcagcct
g4313	taatatttgcaatcctcctacctcagcctcttgaatgctcagaaa
g4358	ccaggcattaacccaagtttctcttctctgggtccctttcttaag
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g4448	agcccatggatctgcactctctaatatgaaatatattgcataaaa
g4493	tgtctggcctcagtttccccacctgtcaggtttaggcagcacagt
g4538	cgggtccaagacacttcattatttgcaggcaggtataagaagaagct
g4583	cccatccccacccgcttcctccgggtccctaagacagaataacttc
g4628	tacactgaaactgaactctcgcagacgcataatgctcactttaatg
g4673	atgatgaaataatgggggaaactgaggctccgagagattcctggag
g4718	gaagaggggtcaaaaccagctccaggaagctctccagcccccatcc
g4763	gggcctctccagggttctggggcttggcgaggagtgaacacagctggg
g4808	aggggctggagcctgggagcttggcccttgctcgtgcccageac
g4853	ctgctgattcttgcacgggagccagcaggcggctgcgtccgcccga
g4898	gagactgaagaagccgggggtaggggttgaggaggaggtaagcaggg
g4943	gctgtggggggccgaagcttgtgccaggggcctgtcagcaggtcccc
g4988	agttttatttatggcgtgaggccgatgtccttatccgctggcctg
g5033	ctgggggatggctgcggctggggattggacccaagggctggcttc

F- F

Fig. 2(6)

F- . - . - . - . - . - . - . - . - F

g5078 ccactcagtcctccageccactccatgtcacacccgtgcattctc
g5123 tgaggcttatcttggaacccgcccttggtctctgtgctgtctgtct
g5168 ctatttctgtcattcactttcccagagccttttttttatgctttt
g5213 aatataactacgttttaaaaattgcttttgtataatgtgtgtgcc
g5258 ttctgtgagcgtgctgcccacacacacacgtgaaggtagagaac
g5303 tttgttgagtaggctcctccaccatgtgggactagggctggcga
g5348 caagagcaattactgagtcattctcgcagccctcaccctcact
g5393 tcccatcctgtttggatagtcataaggtaatcgaaggtaaactcgt
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g5663 ctgatttgactccctcctttgcttgtctccatcgccgtggcattg
g5708 ccattcctctgggtgactctgggtccacacctgacaccttccca
g5753 actttccccagccgaagctgggtctgggtatgggaggccgcccgtccc
g5798 gcgcgcgcctcctgctggccgcgcceccaacactgccgctccattc

g5843 E R P G P G G G V C E P R
tcttttagAGCGCCCGGGCCCGGGCGGCGGGGTGTGCGAGCCGCGG
g5888 G G E P S S G P V R R E L K Q
GGCGGCGAGCCCAGCTCGGGCCCGGTGCGGCGCGAGCTCAAGCAG
g5933 F L G W L K K H A Y C S N L S
TTCCTCGGCTGGCTCAAGAAGCACGCATACTGCTCGAACCTTAGT

G- . - . - . - . - . - . - . - . - G

Fig. 2(7)

G- · - · - · - · - · - · - · - · G

[illegible]

Fig. 2(8)

NOVEL HAEMOPOIETIN RECEPTOR
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H- . - . - . - . - . - . - . - . H

g6428	CTGAATTGGAGCCCCCTCTGTACCATCTGGGCAACAAAGAAACCTA
g6473	CCAGAGGCTGGGCACAATGAGCTCCCACAACCACAGCTTTGGTCC
g6518	ACATGATGGTCACACTTGGATATACCCCAGTGTGGGTAGGGTTGG
g6563	GGTATTGCAGGGCCTCCCAAGAGTCTCTTTAAATAAATAAAGGAG
g6608	TTG TTCAGGTcccgatggccagtgtgtttggggcctatgtgctgg
g6653	ggtgggggga

Fig. 2(9)

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GCGGCCGCTG	CAGTGATTAC	TCACCGCGTG	GCGCACCCCA	CCCGCGGGCC	GCTGAGTGGA	60
TTTTTCCGTG	GGGGGATGTG	AAGAAGTTTA	GGGAGAACTC	TTCTGCACCG	ATGGGAACTA	120
GGAATGCAGG	GTTCGGTCCC	GTTCCCCAA	GGACACACCT	CTCCCCATAA	GCCCACTCAT	180
AAGGGCTCCC	TGCACGCGCT	CCGGGACATC	CCCATATCCA	ATACCCGCAG	ATATGATAGT	240
TGAGAAGGGA	CCAGAGGCCG	GAGACTCCCT	CCCTGCCTTC	TGGCTTTCCC	CCCCCCCCTGC	300
ACGAAACGAG	ACTACAGCGA	TGGAGAGAGT	GGCATGAAGG	CTTAGGGTGG	GGATCGGTAG	360
GACCCATGCA	CCCAGAGAAA	GGGACTGGTG	GCAACTTTCA	AACTCTCTGG	GGAAGGAAGA	420
AGGGCTGAAA	GAGGATGAAC	GGGCTCAGGT	ACTGCTCAAT	GTGTGTGTGG	CGGACCAAAG	480

Fig. 3(1)

A

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A

TGGGTATGGG	GGCCCCGTAA	GAGGGCGGG	GAAGGTGGAT	AGGAAGGATC	CCGGTAGACT	540
GGAGGGGATC	CTGGAAAGC	ACCAGGGCTG	CGAGCTAGGA	ACCCATTCGG	AGTTAAGGCT	600
ACAGGATCCC	AGATGAGGGG	GTGGGAAGCC	TGGACGGGC	GGGACCAGAG	AGGGAGGTCC	660
CACGGGCTGG	TGGGAAAGA	GTGGGGGGCT	TCGCCAGGA	GGATGGGACG	TTCAGGAGTG	720
GTAAGTGGC	GGAGGCCGGC	CGGGCGGGC	GCGCGGTGCC	CGCCGGCGGT	GGGAAGGCCG	780
GTGCGGGGCC	CACGATCAAC	CCCCCCCCCAG	GGGCCGGGCC	GGGCCGGGGG	CGGGGCCCGG	840
CGGGGCGAGC	GGCGCATTAG	CGCCTTGCTA	ATTTCGGCTG	CTCAGACTTG	CTCCGGCCCTT	900
CGCTGTCCGC	GCCCAGTGAC	GCGCGTGAGG	ACCCGAGCCC	CAATCTGCAC	CCCCGAGACT	960

B

Fig. 3(2)

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B

CGCCCCCGCC CCATACCGGC GTTGCAGTCA CCGCCCGTTG CGGCCACCC CCATGCCCGC 1020

GGTCGCCCCG GGCCCCGTCG CCCAATCCGC GCGCGGCCG CCGCGGCCG TGTCCCTCGT 1080

GTGGTCGCCT CTGTTGCTCT GTGTCCCTCGG GTGCCCTCGG GCGGATCGG GAGCCCGTGA 1140

GTACCGTGCG CCTGCTCCC CACCTCCCCA GGGAAGCCGG GATCCGGCGC CCCGGGGGT 1200

AGTCGCGGGG GATGGAAGAA GGGGCGCGAG CGCCACCTGG ACGTCCCGGG AACAAAGGAA 1260

GGCGGCCCTC GGGGCGCCCT CACCTGTGGG GTCATGGCA CCACCACCCA GCCTCCCAAG 1320

C

Fig. 3(3)

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Fig. 3(4)

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D		
CGAGAGCAAG	CGTGTCCGGG CACCGCGAGC CCAGACTTCA TTGTCTAAGG GGCACCCAGT	1860
GGGGGTCAGC	TGCCGAGAGA ATCCCACTGT CCCAGGAGGA ACTCCTGGCC TTGAGCCCCC	1920
ATCACCCAAC	GCACACATCC CCGCCAGGAT GCGGTCTCCA CATCCAGACC CTCTCTGGGA	1980
CACACCCAA	GACACACAA AGAGCCCCAC TGGCTTATGT CCCGTCACCC TGCCCTCCGA	2040
CGCGCGCTGC	AGCCCAGATG CGTATTCGCA CACCATCGCG GCGCTCGCAT TCCATCCTCT	2100
ACACACACAC	ACACACACAC ACACACACAC ACACACACAC ACACACAGAC ACGCACACAC	2160
ACACGCACGC	ACACACACGC ACGCCCGCAC TCGTGGTCCC ACATTATTTT CACAGGGGAG	2220
GCACACCCGG	GGTACGCATA TGGTTGAGTG CACTGGAGAT CTTTCCCCAC CACTCTCAGG	2280
E		

Fig. 3(5)

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Fig. 3(6)

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F		
GAGGCCACCT	TCCCGTTGGC	CTTTCAGGGA ATCTCACACT TTTCCCTTTT AAAACACATG 2820
GTGTTCTTTT	TAATAACGGC	AGCAACTCCG CATTGGGAAA GGGGAAATA AGCTTGATA 2880
GGCCCCGGCT	TTGTGGAAG	GAGGGAAGA GGAAGAAA AAGAGGGGT GTCTCCTCCA 2940
GGCTTAGGGG	GCTGTCAGCT	GCTGCTCTGT CTAGCTTGGC ATGTGTGTGC CCCAGTCCCC 3000
AGTGGCTTTG	GCCCATTTGT	TGTGAAGCC AAGAGGGAGA CTGGAGTCCT CTATCTCTGG 3060
TACTCCAGAG	TCAGGCTTCT	CAGTCCGAGC CCAGAGAAGC TCTTCCCTGT TTTATGGAGG 3120
GAATCAGGGA	AGGGGGTGCC	AGGTGACTA CGTTCTGCTG AGGACTGTAC CAGTCGCTCG 3180
AAGGAGAAAG	CTTGGGCTTG	CCCCCCTCCC CCTCAAGCC ACGAAGGGCA GCTGCTAGGC 3240
G		

Fig- 3(7)

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G		
TAGTGTGGTA	AAAGGCATT ACTCCCCAGC CAGGACCCCC CAGAGAGTCC CCTTCCTGGC	3300
CAGACAAATG	CTGGGGAGGG ACAGAGGGGT GTGATCATTG CCCAGGAGTG CAGACAGTGG	3360
GGTCCCCGGT	CGGGCAGTGC CTCCCCACCCT GCTGAGGGGG GCGCCCAGGC AGGAAGCGGT	3420
GGGTGGGCCG	GGGTAGAGAC GCTGGCACGT CCCAGTTCAT GCCGAAGGAA TTCTGAATTA	3480
GCGGGCGGCT	GGCTGCCCTGG GACCTCCGGG GCGGCCCCCT GGCCCCCGCC GCTCCGTCCTG	3540
GCCTGCTCCT	CCTGCTCCTT CGCACGGACG CTGAGACCTC CGCTGAGCCC TGGGACAAGC	3600
CCCAAATGCA	ACTGCGATTG CAGGCTTCGC AAGACCCGCC TCCTCCCAAG GCCAAATTG	3660
CCTGGGAGAA	GTCATTCAGG GCCCAGACTA GAACCATGTT GGTGCCACCT CATCCATCTG	3720
H		

Fig. 3(8)

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H	
3780	GGCATGAAG GACCGTCCAG GGCTGCAGTT TAGCTTCTTA ATAGGAACCT GGGGTGGGT
3840	ACAGCCTCTG TTCTCCGAGC CTCTTTGGAA ATCGGTTTIG TTTTGTGTTT TGTTTTTC
3900	AATACTCTT TCCTCTCATC CCATCCCGGG ACTGTGTTCC TCCCTAAGG TTGAGAGCCC
3960	GCAGTCTTC CCTAACCTT TCATTGCTC TACCCAGG CCTTGCACA TGGAGTCCCA
4020	CTCTCCCCCT TGCCCAACTG GGGCTCCAGC CTACTGCAT TTGGCTCTG GTAAGTGTCC
4080	AGGGCCTCT CTGACACACA GGTGTAGC CCCAGCTCC TCTCTCTCC TCCCCCTTT
4140	CTCTTTTGCT TCTGAGACTT AATTMTTC TTTTCTTTT TGGCTTTTG AGACAGGGT
4200	TCTCTGTACA GCCCTGGCTG CCCTGGCACT CATCTGTAG ACCAGGCTAG CCTCAAACTC

Fig. 3(9)

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ACAAACCTAC	CTGCCCTCTGC	CTTTCAGTG	CTGGCACTAA	AGATGTGGGC	CACCACAACT	4260
AGTAGTTAAG	TGTTTTGCTG	TGTCTTTATT	CCTATAGTGA	CCTCAGTTCC	TGGCATATTG	4320
TAGGCGATGG	ATGGATGAAT	GGATGGATGG	ATGGATGGAT	GGATGGTTGG	ATGGAGCAAG	4380
CTTGAATCGT	CCTGAGTGAA	AAAAGAGACC	TCAGAGAACT	GAATGGAGTT	AGGTTCCCAG	4440
GGCAGCCTGG	CCTGCTGGTC	TCATGGGAGC	TCCCTGTGAA	ACTTCCCCCA	CACCTCCCAC	4500
CACCCTGCCA	TCCTGTGTGG	CTGACAAGAA	AGGCCAATGG	CCAGATGGGG	ACACAGACTC	4560
AGGGAAGCTT	GGAATATGTT	CCCCTCCTCA	TATCCTAGGC	CTGTGTGTCC	CCCTGAGGGC	4620
CCAGCCTATG	AGTAGGGCAG	CTGTGGGCTG	CCCTAAGGTT	GGGTAGGCAA	GAAGGGGTG	4680

Fig. 3(10)

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Fig. 3(11)

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K

TGGCTTATGT GTAATCCCAG AACTCTGGAC GCTGAGGCAG GAGGATTCCA AGTTTCAAGA 5220

CAGTGTGTC TAGGTAATGA GACCCTGTCA AGAAAGAAA AGAATAAAG AGACAAGAAA 5280

ATGTTTATAG GCTGTGAGAC AGCTTGGTGG GTAAGGGCA CTGCTCTCCA ATCAAGATGA 5340

CCTCAGCCCC ATCCCTAGGA ATCCATGGTA GAAGAGAAA GCAAACTCCA GCTGCTGACC 5400

TCATACATG TGCTCCAATG TGCACACACA CAGGAGACA TAATCAATTA ATAGGATGTA 5460

TTGCTTAGA TTGAGTAGG CATTATGAC TGATGTTTA AAATTTTAT TTGATTTTAT 5520

AAAAATATAC CTGTTGTAT TTGGTTGGT TTGGTTGAG TTTTGTAT TTGAGACAGG 5580

CTTCTCTGT GTAGTCCTGG CTGTCCCTGG AACTCACTCT GTAGACCAGG CTGGCCCTGA 5640

Fig. 3(12)

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Fig. 3(13)

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Fig. 3(14)

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N						
CTATGTTGGC	TGTAAGTGGG	GCCCCAGACA	CTCAGAGATA	GATGGGGGTT	GGCAATGACA	6660
GATTAGAGC	CTGGGTCTTC	TGTCCTGGGG	CAGAGCCATG	GGCTCTCACT	TGCATGCAGG	6720
CATGGTCATA	CCCAGCACAG	GCATTGCAAC	TCTAGGGACA	GCTGTGGCTG	CACGTGCCCC	6780
TGTGTACCCC	ACAGCTTTAG	AAAAGCTGTC	ATGTTTTCCT	TGTAGTGCCC	CCTGAGAAGC	6840
CCTTTAACAT	CAGCTGCTGG	TCCCCGAACA	TGAAGGATCT	CACGTGCCCG	TGGACACCCG	6900
GTGCACACGG	GGAGACATTC	TTACATACCA	ACTACTCCCT	CAAGTACAAG	CTGAGGTTGG	6960
TACCCAGCCA	AGCCTTGCTG	TGTGACTTCT	GGCAATACTT	ACCTTCTCTG	ATCAAAATATG	7020
TTCTGTGTTA	TGAACTCAA	AGGGACTCTC	GCACCTCCAC	AGGTGGTACG	GTCAGGATAA	7080
						O

Fig. 3(15)

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O

CACATGTGAG	GAGTACCACA	CTGTGGGCCC	TCACTCATGC	CATATCCCCA	AGGACCTGGC	7140
CCTCTTCACT	CCCTATGAGA	TCTGGGTGGA	AGCCACCAAT	CGCCTAGGCT	CAGCAAGATC	7200
TGATGTCCTC	ACACTGGATG	TCCTGGACGT	GGTGAGCCC	CCAGTGTCCA	CCTGTGTTCT	7260
GCCCTAGACC	TTATAGGCG	CCTCCCCCCC	ATCCCCCAG	ACTTTTGGT	TCTTCTAGAG	7320
GTCTTAGCCA	CAGCCACGGT	GGTTGCAGGA	CAGTGGTTGT	TCATAACTTA	ATGCAAAGAC	7380
TTTCCCCCAA	GACAGTCAAG	ATTTTCCCCCT	CCCCACCCCC	AACACACACA	TACACACACA	7440
TCTGCAGAG	AACACCTGGC	CTGACCACCC	TCCCTCTCTA	CAGCCCAGGT	GTTCAGAAGG	7500
TAGTCCTAGG	GGA CTGAGAG	GAGGCGCCCA	GGTCTGAAGG	CGCCCCAGGA	AGCCGAGGCC	7560

P

Fig. 3(16)

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P		
	TTGAGCTGGG GGGGGGGCG AGGGTTGGAG GCACGAACTG GATGATCCCT GAGCACAACT	7620
	GGCCCTAATC TAATTAGGGT GTTCCCAGCC CAAAGCAGCC TGGGCCATT T AACCTTCAA	7680
	GTGCCCTCACT GAAGACTCAG GGGAGAGATC AGCTTGACT CTCTCCATGG TCCCCCAGGA	7740
	GGTTCCTGG GTGCCCTGG CTCATTCCA CATCCAGAGG TTTGTGTCT TCCCTGGCATC	7800
	AACCTCAG TTGTGCTCTG TGGCTGGCAC AGCTGCCCCG TGGAGGCTCT TGGTAATGTA	7860
	AAGGCATCA GAGGTGGACA TGGGATGGG ATACATAGG ATGAGCCAA ATAGCACCTC	7920
	AGGTGGGT GATATACAAT AAAGCTTGTC ACCCTGACGC TCAGAAAGCC TACTCATGAT	7980
	ATCACAATT GTTGACATCA CTCTGGGACA TGAGTGAGA CCTAGCTCA AAACACAGAC	8040
	Q	

Fig. 3(17)

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Fig. 3(18)

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R		S
8580	AGCTCCAGGC CAGCCAGGGT GCGCAGTAAA ACCTTGCTCTC AAAAAACAAA GCATCTTTAG	
8640	AGACCAGGCT TGCTCCACCC CCAGTGACCA CGGACCCCCC ACCCGACGTG CACGTGAGCC	
8700	ACGTGCGGG CCTGGAGGAC CAGCTGAGTG TCGGCTGGGT CTCACCACCA GCTCTCAAGG	
8760	ATTTCCTCTT CCAAGCCAAG TACCAGATCC GCTACCGCGT GGAGGACAGC GTGGACTGGA	
8820	AGTGCCCCGT CCGCCCCCGG ACCCGCCCCCT GACCCCCGCC CCCGCATCTG ACTCCTCCCT	
8880	ACCGTGACG GTGGTGGATG ACGTCAGCAA CCAGACCTCC TGCCGTCTCG CCGGCCCTGAA	
8940	CCCGGCACC GTTTACTTCG TCCAAGTGCG TTGTAACCCA TTCGGGATCT ATGGGTCGAA	
9000	AAGGCGGGA ATCTGGAGCG AGTGGAGCCA CCCACCGCT GCCTCCACCC CTCGAAGTGG	

Fig. 3(19)

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TGAGCACCTC	TCCAGGGCTG	GCTGGCCCAT	GGAATCCCA	ATCCATCCTG	TTCTTCCCC	9060
CCCACCCCTT	TTTTGAGACA	GCGTCTTCAG	GTAGCGCATG	CTGGCCTAA	ATTCAGTATG	9120
TAGTCAAGGA	TGACCTCGAG	CTCCTGGTCT	TTTTGTCTCC	ACTTAGAGAC	AATGGCCAGT	9180
GGCCATCACC	ACCTTTGGGA	GACTAGCCAT	GGAGTCTATT	TAGCCTGTCA	TTTGGTGACA	9240
GATGGAGTAC	AACAGTGTGA	CCTCTGTAA	GAGAACTGAA	GACAGGCTGT	TTTTAAACCCC	9300
AATATCCTAG	GCTCTCTAGA	GGTTAACTTT	ATATAAATA	GAGACTATTA	CAGCCAGTTA	9360
TCACATGGTC	CCACAGAACC	TTTTGTGACA	CAACCTATAG	ACCACAGTGC	CTGTGCCCTAC	9420
CACATAAGGG	TCTCTACTGC	TGGCCACCCC	CTCCAACCCT	TAAAAGGTAA	CCTAGGCAGC	9480

Fig. 3(20)

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CTTAATATT	GCAATCCTCC	TACCTCAGCC	TCTTGAATGC	TCAGAAACCA	GGCATTAAACC	9540
CAAGTTTCTC	TTCTCTGGGT	CCCTTTCTTA	AGGTGGGAGG	GCCTAAAGAT	GACTTCCTTT	9600
GTCCTGAAGA	CTCTCCGAGC	CCATGGATCT	GCACTCTCTA	ATATGAAATA	TATTGCATAA	9660
AATGCTGGC	CTCAGTTTCC	CCACCTGTCA	GGTTAGGCA	GCACAGTCGG	TCCAAGACAC	9720
TTCAATTATT	GCAGGCAGTA	TAAGAAGAAG	CTCCCATCCC	CCACCCGCTT	CCTCCGGTCC	9780
CTAAGACAGA	ATACTTCTAC	ACTGAAACTG	AACTCTCGCA	GACGCATATG	CTCACTTTAA	9840
TGATGATGAA	ATAATGGGA	AACTGAGGCT	CCGAGAGATT	CCTGGAGGAA	GAGGGTCAAA	9900
ACCAGCTCCA	GGAAGCTCTC	CAGCCCCCAT	CCGGCCCTCT	CCAGGTTCTG	GGCTTGGCGG	9960

U

Fig. 3(21)

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Fig. 3(22)

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V						
GTGCCACAAC	ACACACGTGA	AGGTTAGAGA	ACTTTGTGTA	GTAGGCTCCT	TCCACCATGT	10500
GGGACTAGGG	CTGGCGACAA	GAGCAATTAC	TGAGTCACTCT	CGCCAGCCCC	TCACCCCTCA	10560
CTTCCCATCC	TGTTTGGATA	GTCATAGGTA	ATCGAAGGTA	AATCGCTGGC	TTTAAATTTCG	10620
TAGCTATCCT	GCCTCAGCCT	ACCAAGTGCT	GTGCTACCAC	GTTTGTGGGA	GGGGCTCTCC	10680
TCCCAGTGTC	TGGGGGTACA	CAGTCCCAAG	ATCTCTGCTT	TCTAGGTCTT	TGTCTTAGTT	10740
TGCCCCCTTGC	TTTGTCCGTG	TCCCTAGAGT	CTCCGGCCCC	ACTTAGTCTC	CATTGATTTC	10800
CTTTCTGACC	GAATACTCGG	TTTTACCTCC	CACTGATTTG	ACTCCCTCCT	TTGCTTGTCT	10860
CCATCGCCGT	GGCATTGCCA	TTCTCTCTGG	TGACTCTGGG	TCCACACCTG	ACACCTTTCC	10920
W						

Fig. 3(23)

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W
10980
11040
11100
11160
11220
11280
11340
11400
X

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X

CCTTCCCCCT	CCTTCGGTGT	TGCTCAAAGG	GATCTCTTAG	TGCTCATTTC	ACCCACTGCA	11460
AAGAGCCCCA	GGTTTACTG	CATCATCAAG	TTGCTGAAGG	GTCCAGGCTT	AATGTGGCCT	11520
CTTTTCTGCC	CTCAGGTCCT	GCCGGCTAAA	CTCTAAGGAT	AGGCCATCCT	CCTGCTGGGT	11580
CAGACCTGGA	GGCTCACCTG	AATTGGAGCC	CCTCTGTACC	ATCTGGGCAA	CAAAGAAACC	11640
TACCAGAGGC	TGGGCACAAT	GAGCTCCCAC	AACCACAGCT	TTGGTCCACA	TGATGGTCAC	11700
ACTTGATAT	ACCCAGTGT	GGTAGGGTT	GGGTATTGC	AGGCCCTCCC	AAGAGTCTCT	11760
TTAAATAAAT	AAAGAGTTG	TTCAGGTCCC	GATGGCCAGT	GTGTTTGGGG	CCTATGTGCT	11820
GGGGTGGGG	GA					11832

Fig. 3(25)

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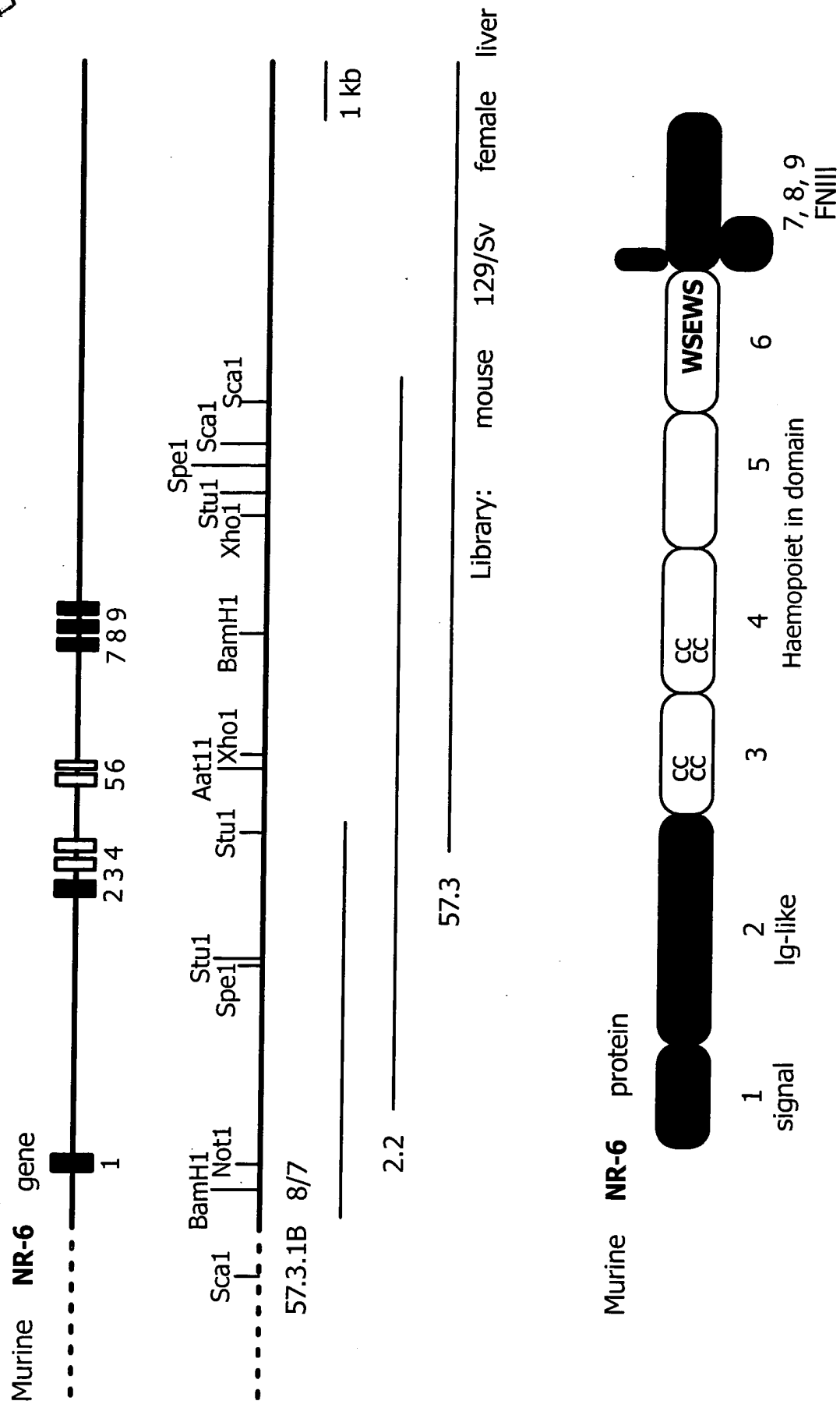


Fig. 4

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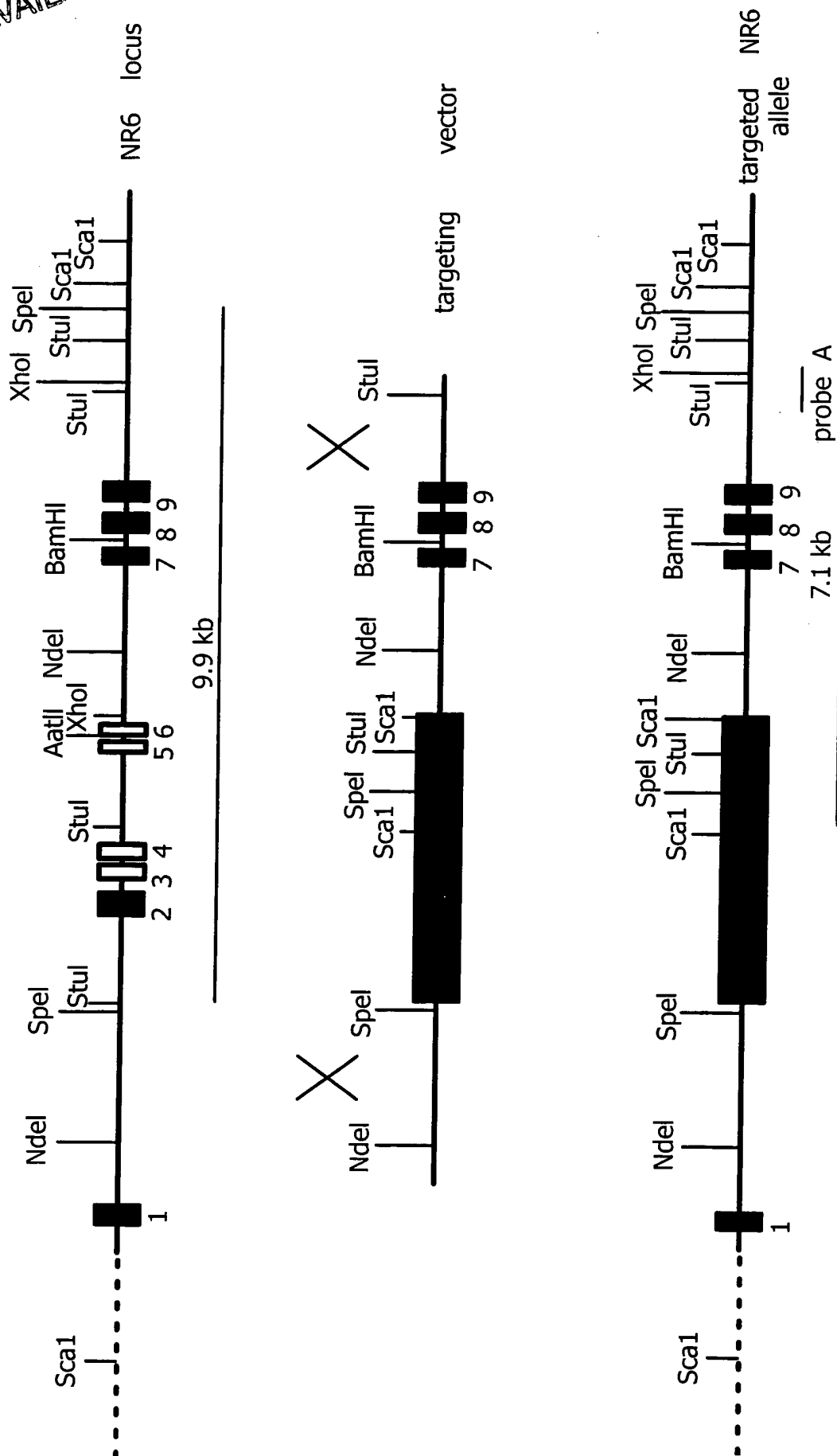


Fig. 5

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A A

1 ATGCCCGCCGGCCGGCGGCCCGCCCGCCCAATCCGGCGCGCGCGCCG

1 ATGCCCG

79 GTCCCTCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG

91 GTCCCTCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG

169 GCCACCTGCTCAGTGCACGGAGACCCACAGGAGCCACCGCCGAGGGCCT

181 GCGACCTGCTCAGTGCACGGAGACCCACAGGAGCCACCGCCGAGGGCCT

259 TCCCGTGTAACAAGCCCTCCACCTTGGCTCTGGCCCTGGCCAACTCAA

271 TCCCGTGTAACAAGCCCTCCACCTTGGCTCTGGCCCTGGCCAACTCAA

349 GCCCGTGACGGCAGCATCCTGGCTGGCTCCTGCCTCTATGTTGGCCTGCC

361 GCCCGTGACGGCAGCATCCTGGCTGGCTCCTGCCTCTATGTTGGCCTGCC

439 ATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGGAGACCTT

451 ATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGGAGACCTT

529 TATGGCCAGGACAACACATGTGAGGAGTACCACACAGTGGGCCCCACTC

541 TATGGCCAGGACAACACATGTGAGGAGTACCACACAGTGGGCCCCACTC

B B

Fig. 6(1)

A	G---CCGTTGCTGCCCCCTG-----CTGCTGCTCTGC	Human NR6
	CGGCGCGTGTCCCTCGCTGGTGCCTCTGCTGCTCTG	Mouse NR6
	TCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTG	Human NR6
	CCCCCAGGAGCCCACTTCTCATCGGCTCCTCCCTGCA	Mouse NR6
	CTACTGGACCCCTCAATGGCGCGCCTGCCCTGAGCTC	Human NR6
	CTACTGGACCCCTCAATGGCGCGCCTGCCCTGAGCTG	Mouse NR6
	TGGGTCCAGGAGCGGTGCGGGGACAACTCGTGTGCCAC	Human NR6
	TGGGTCCAGGAGCGGTGCGGGGACAACTCGTGTGCCAC	Mouse NR6
	CCCAGAGAAACCCGTCAACATCAGCTGCTGCTCCAAGAAC	Human NR6
	CCCTGAGAAACCCGTCAACATCAGCTGCTGCTCCAAGAAC	Mouse NR6
	CCTCCACACCAACTACTCCCTCAAGTACAAGCTTAGGTGG	Human NR6
	CTTCACTACCAACTACTCCCTCAAGTACAAGCTTAGGTGG	Mouse NR6
A	CTGCCACATCCCCAAGGACCTGGCTCTCTTACGCCCTAT	Human NR6
	ATGCCAATATCCCCAAGGACCTGGCTCTCTTACGCCCTAT	Mouse NR6
	C-----C	

Fig. 6(2)

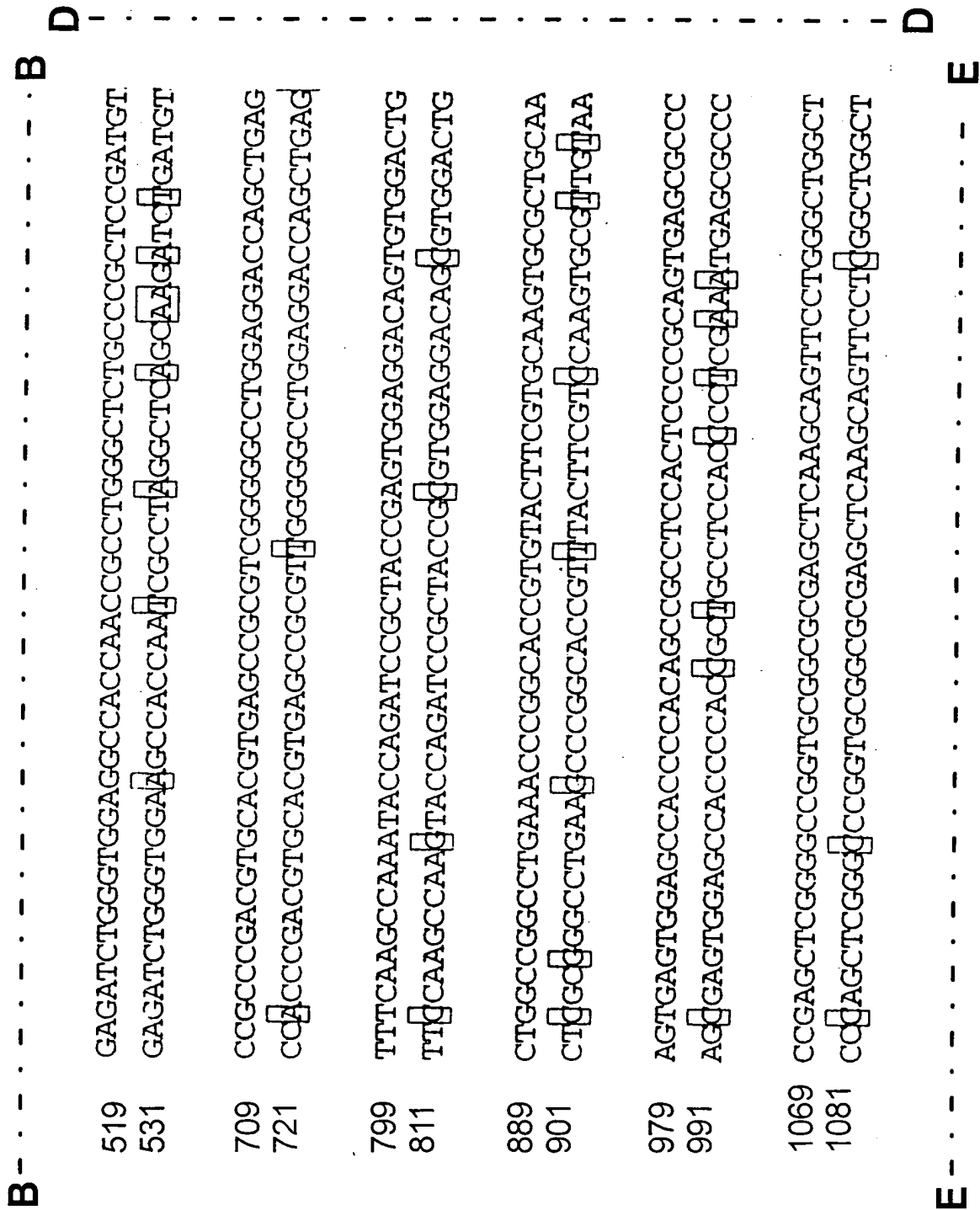


Fig. 6(3)

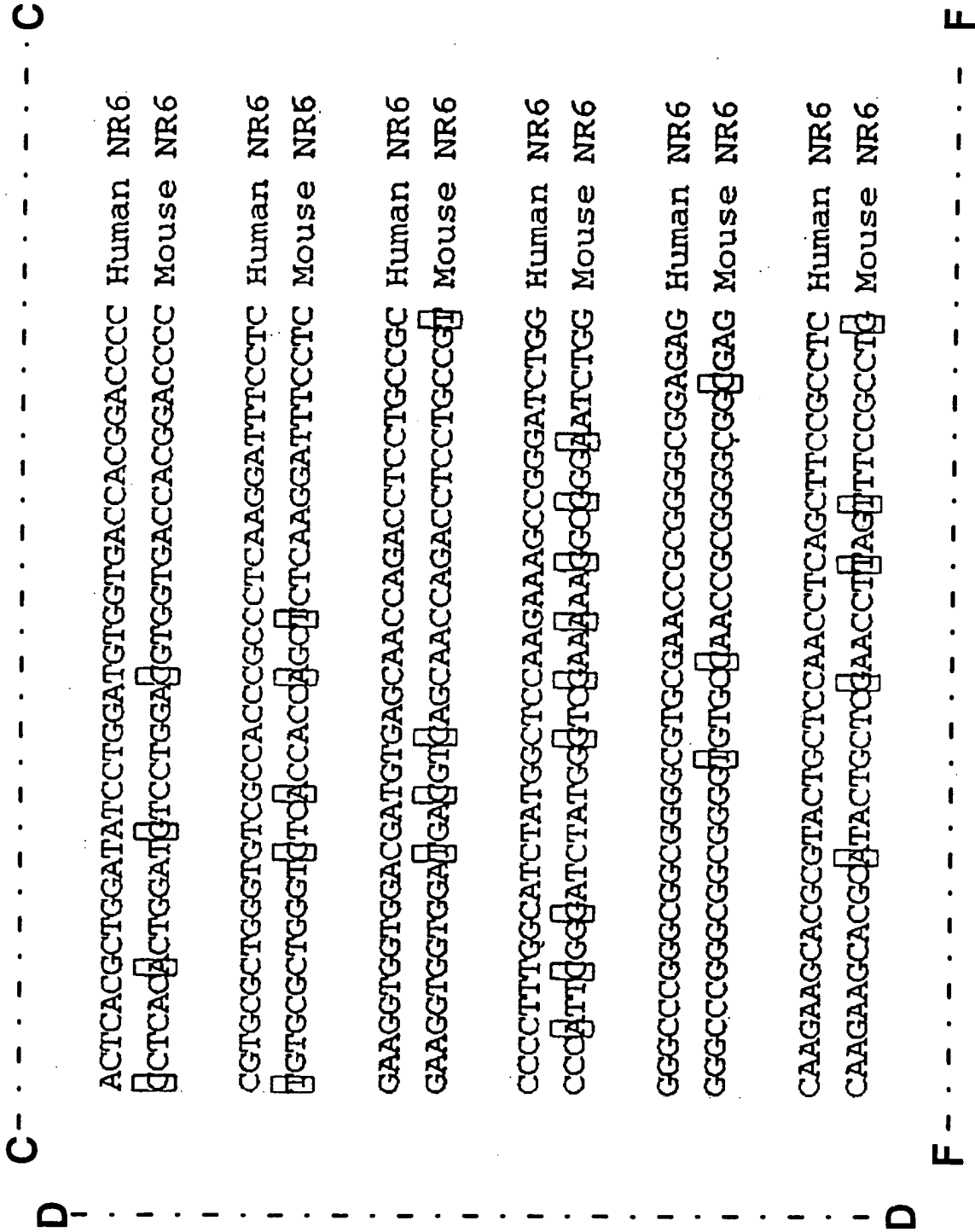


Fig. 6(4)

F-----F G-----G

1159 TACGACCAGTGGCGAGCCCTGGATGCAGAAAGTCGCACAAGACCCGCAACCA
1171 TACGACCAGTGGCGAGCCCTGGATGCAGAAAGTCGCACAAGACCCGCAACCA

1249 AGAGGTCTTCCAGATAAGCTGTAGGGGCTCAGGCCACCTCCTCCCTGCCAC
1261 AGAGGTCTTCCAGATAAGCTGTAGGGGCTCAGGCCACCTCCTCCCTGCCAC

1339 GTACCCCTCACTTCAGGGCACCTGAGCCACCTCAGCAGGAGCTGGGGTGG
1351 TCTGGGCACAAAGAACTTACCTAGAGGCTGGGGCACAAATGAGCTCCCCAC

1429 TGAGGCCACCTTTGGGTGCACCCAGTGGGTGTGTGTGTGTGTGAGGG
1441 ACCCCAGTGTGGGTAGGGTGGGGTATTCAGGGGCTCCCAAGAGTCTTC

1519 AGAAGGGAGTCATTACTCCCCATTACCTAGGGCCCCCTCCAAAAGATCC
1504

Fig. 6(5)

F-----F

G-----G

GGACGAGGGGATCCTGCCCTCGGGCAGACGGGCGACGGCG	Human NR6
GGACGAGGGGATCCTGCCCTCGGGCAGACGGGCGACGGCG	Mouse NR6
GTGGAGACGCAGAGGGCCGAACCCAACTGGGGCCACCTCT	Human NR6
AGACCTGGAGGCTCACTGAAATGGAGCCCCCTCTGTACCA	Mouse NR6
CCCCTGAGCTCCAACGGGCCATAACAGCTCTGACTCCACG	Human NR6
AACCAAGCTTTGGTCCACATGATGTCACACTTGGATAT	Mouse NR6
TTGGTTGAGTTGCCCTAGAACCCCTGCCAGGCTGGGGGTG	Human NR6
GTGTGCCGAATTC	Mouse NR6
	Human NR6
	Mouse NR6

Fig. 6(6)

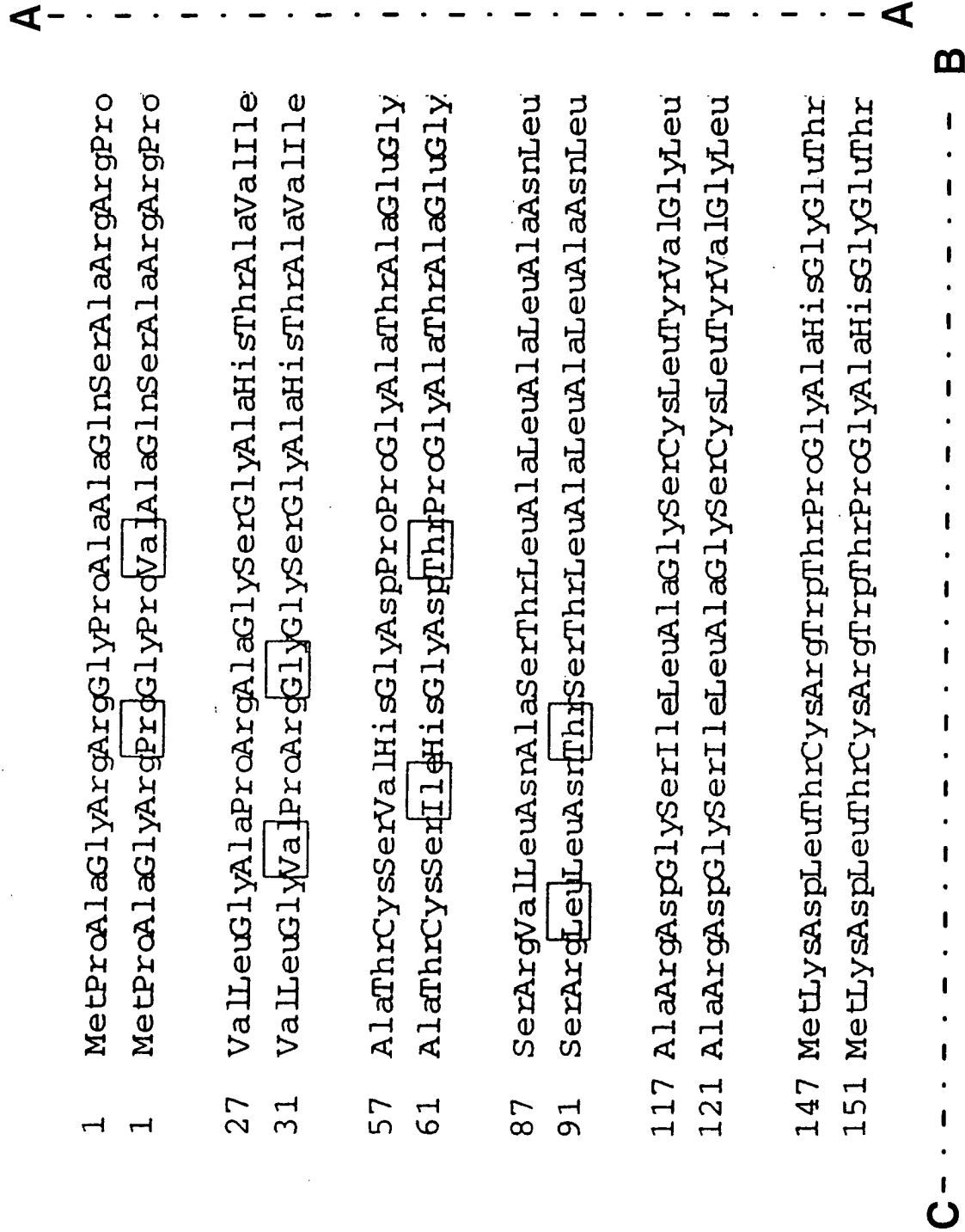


Fig. 7(1)

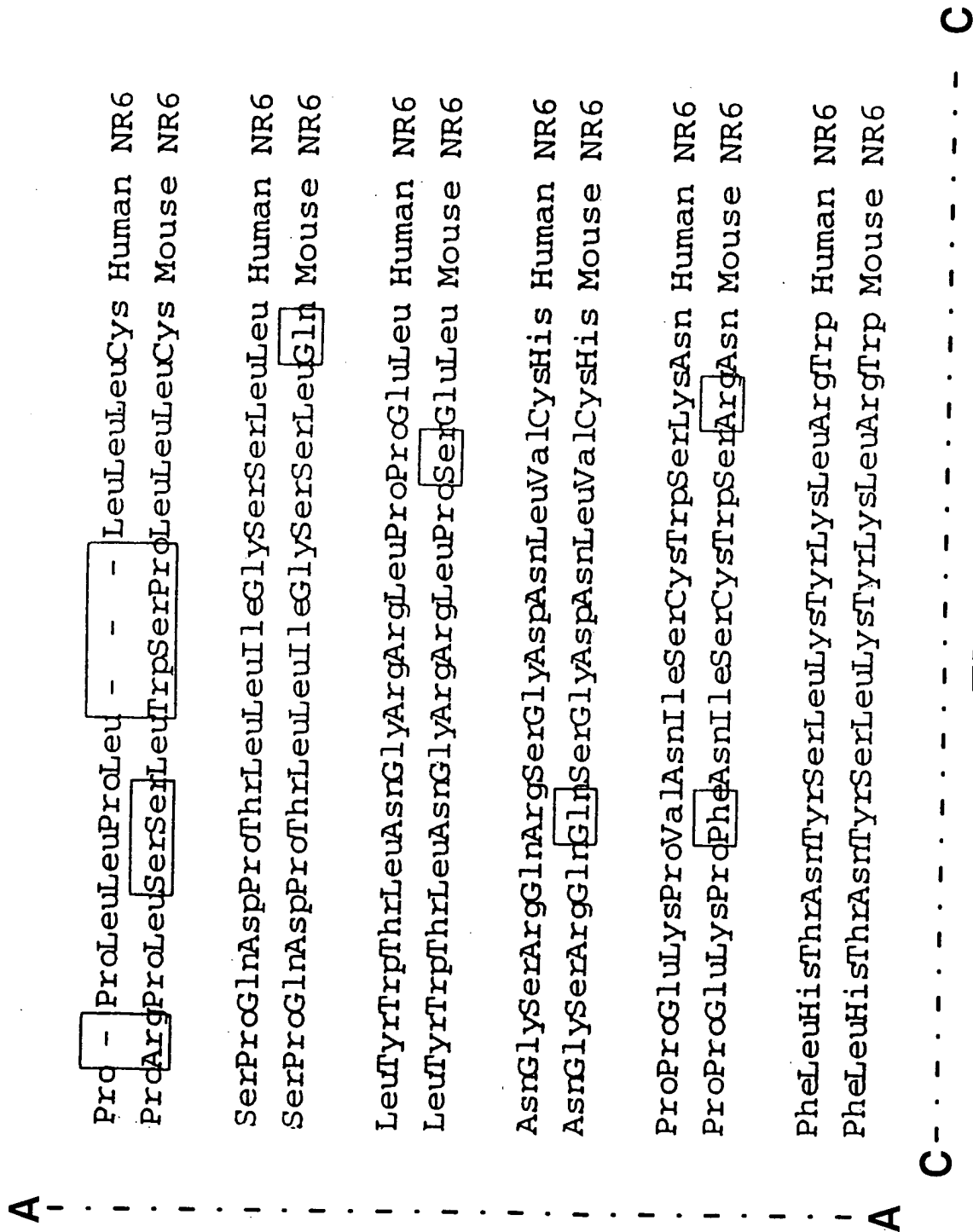


Fig. 7(2)

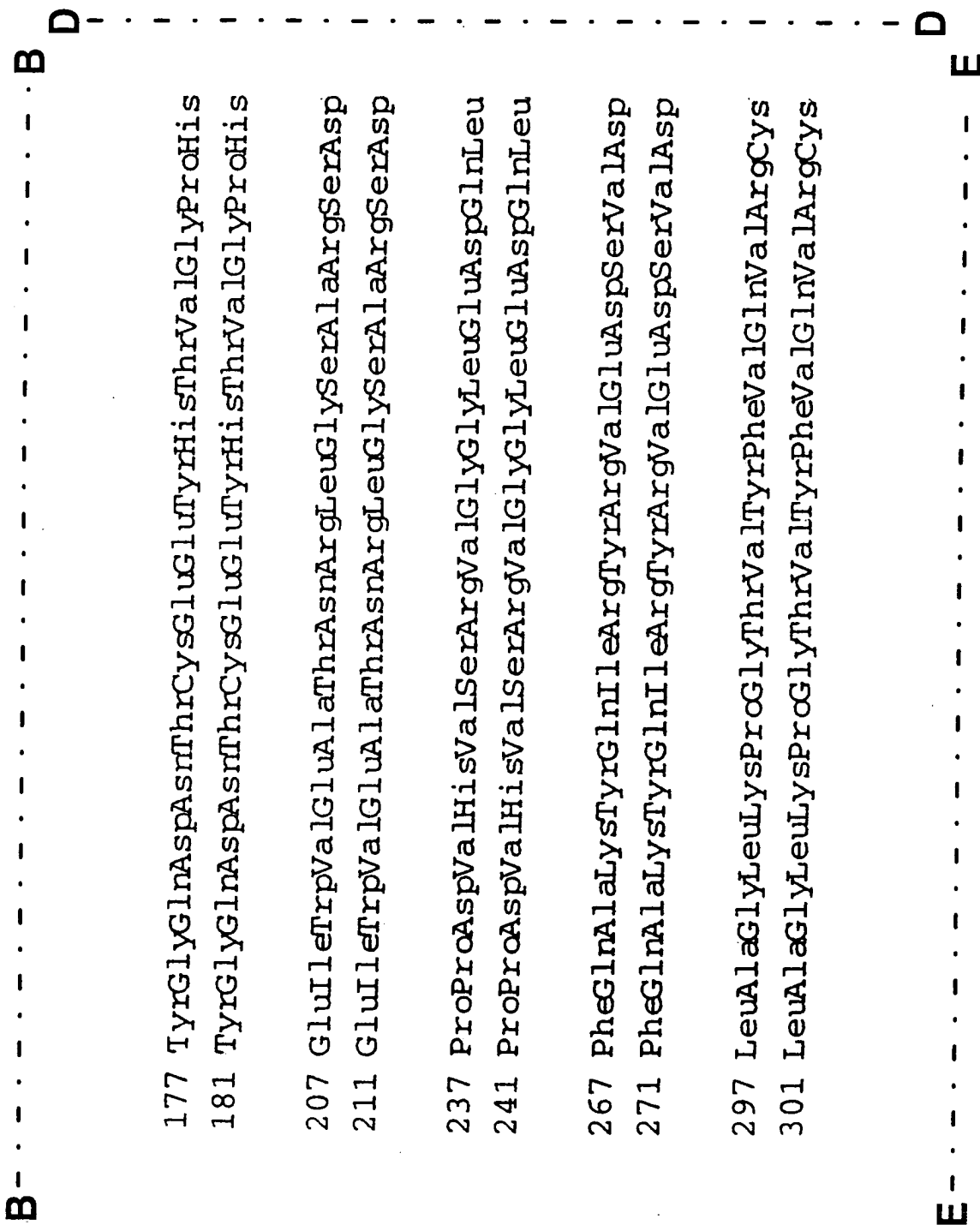


Fig. 7(3)

D	B-----B	
	SerCysHisIleProLysAspLeuAlaLeuPheThrProTyr Human NR6	
	SerCysHisIleProLysAspLeuAlaLeuPheThrProTyr Mouse NR6	
	ValLeuThrLeuAspIleLeuAspValValThrThrAspPro Human NR6	
	ValLeuThrLeuAspValLeuAspValValThrThrAspPro Mouse NR6	
	SerValArgTrpValSerProProAlaLeuLysAspPheLeu Human NR6	
	SerValArgTrpValSerProProAlaLeuLysAspPheLeu Mouse NR6	
	TrpLysValValAspAspValSerAsnGlnThrSerCysArg Human NR6	
	TrpLysValValAspAspValSerAsnGlnThrSerCysArg Mouse NR6	
	AsnProPheGlyIleTyrGlySerLysLysAlaGlyIleTrp Human NR6	
	AsnProPheGlyIleTyrGlySerLysLysAlaGlyIleTrp Mouse NR6	
D	E-----E	

Fig. 7(4)

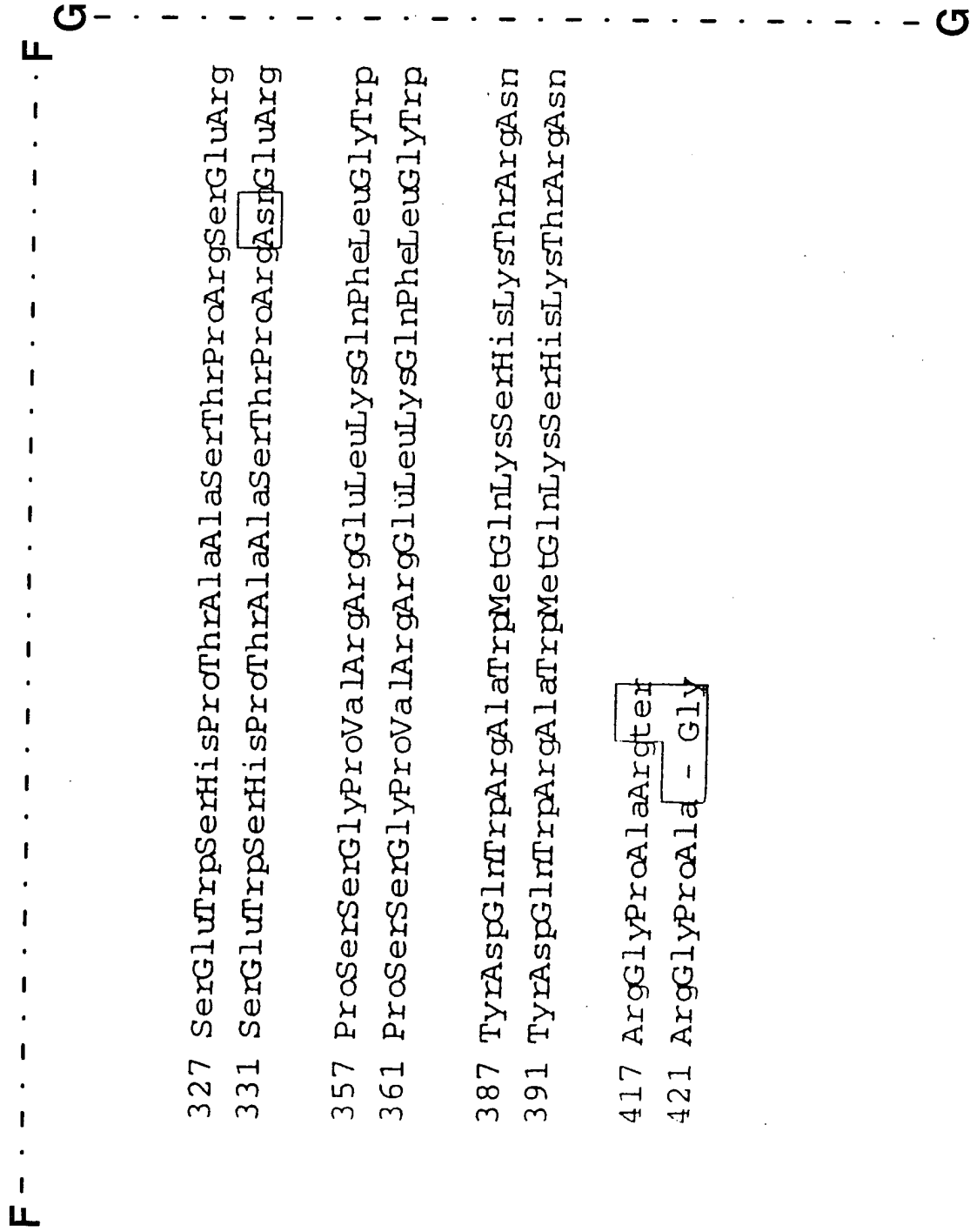


Fig. 7(5)

F-----G

ProGlyProGlyGlyGlyAlaCysGluProArgGlyGlyGlu	Human NR6
ProGlyProGlyGlyGlyValCysGlnProArgGlyGlyGlu	Mouse NR6
LeuLysLysHisAlaTyrCysSerAsnLeuSerPheArgLeu	Human NR6
LeuLysLysHisAlaTyrCysSerAsnLeuSerPheArgLeu	Mouse NR6
GlnAspGluGlyIleLeuProSerGlyArgGlyThrAla	Human NR6
GlnAspGluGlyIleLeuProSerGlyArgGlyAlaAla	Mouse NR6
	Human NR6
	Mouse NR6

Fig. 7(6)

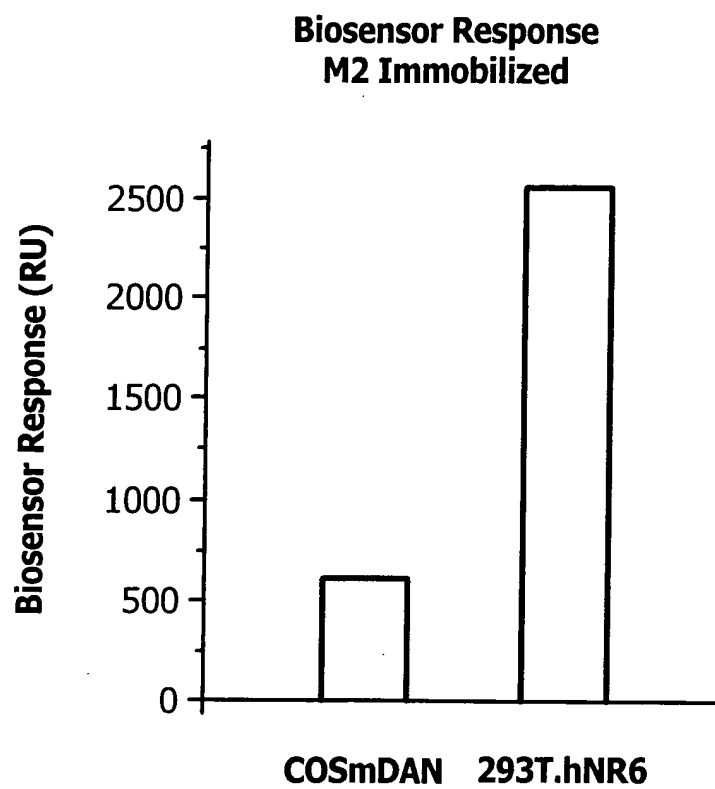
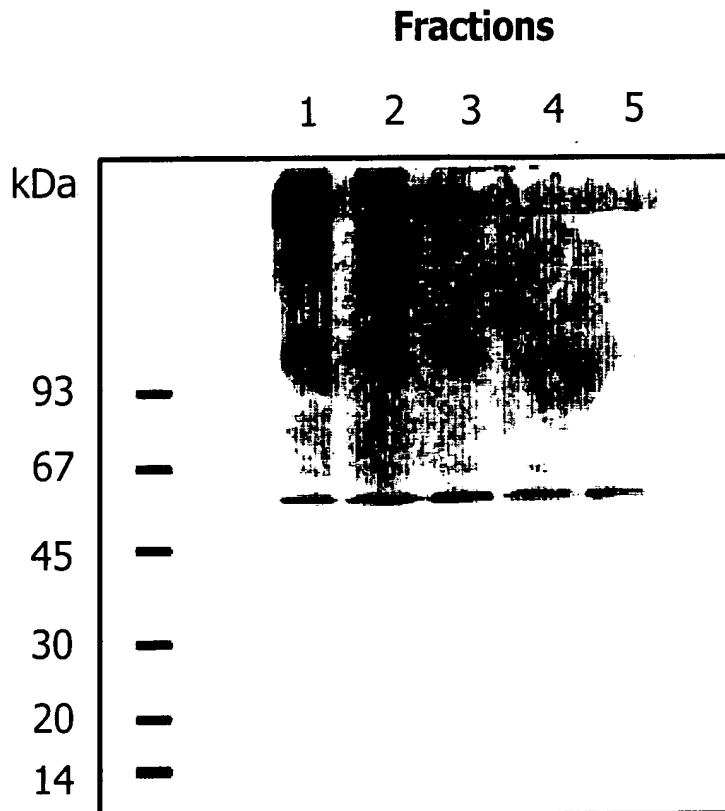


Fig. 8(a)

SDS PAGE/Silver Staining Analysis of M2 Eluted Fractions

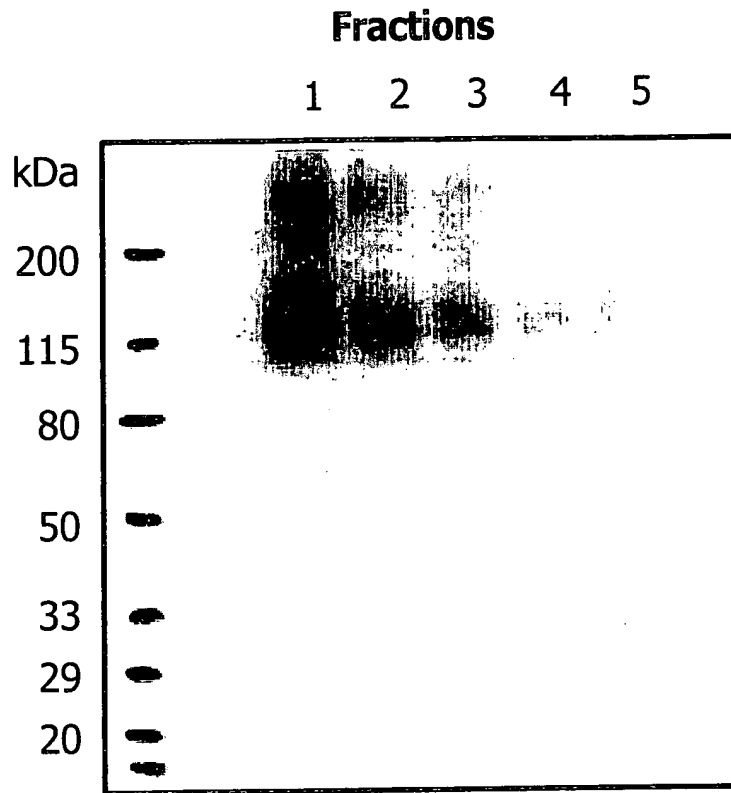


SDS PAGE Conditions:

Gel:	Novex gel 8-16%
Sample buffer:	Non reducing
Silver staining:	Automated silverstain Modified for automation

Fig. 8(b)

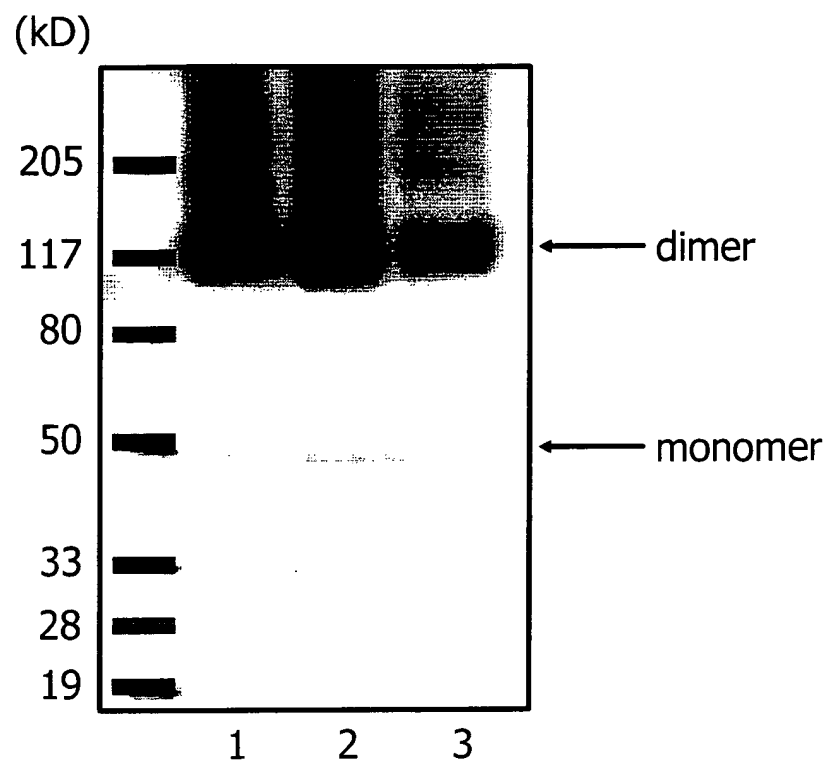
Western Blot Analysis of M2 Eluted Fractions



WESTERN Conditions:

Gel:	Novex gel 8-16%
Sample buffer:	Non reducing
Transfer:	25mM Glycine, 192mM Glycine, 20% MeOH
Transfer conditions:	100V, 1 Hour
Blocking buffer:	1% non fat skim, in TBS Overnight agitation, cold room
1' Ab:	1:500 in TBS 1hr, RT
Wash:	6x5min
2' Ab:	Streptavidin Peroxidase 1:5000 in TBS 1hr, RT

Fig. 8(c)



Biosensor Response

Lane 1: CHO C' FLAG human NR6 clone #30
Lane 2: CHO N' FLAG human NR6 clone #23
Lane 3: 293T C' FLAG human NR6 clone #38

1577 Units
2141 Units
Not Determined

Fig. 9